

Table 1

3. Permutation table

Protein	Seq Possible deletions ID (AS position/AS number)	Insertion positions (Ω) of the inserts (AS position/Seq ID) bridge compos. 1, 2, 3 native bridge compos. 1 epitopes (seq ID 1-3) (seq ID 4) (seq ID 5-36)
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Table 2

2. Amino acid sequences

Seq ID	Amino acid sequence	Seq ID	Amino acid sequence
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Legend : X = D or E
 "- " = an arbitrary amino acid

Fig. 1

1. Amino acid sequences (single letter amino acid code)

Legend: [or] = beginning or end of a possible deletion
 +A/B+ = possible insertion positions of an AA sequence with the Seq ID A
 and/or B

Fig. 3

3. Permutationstabelle

Protein	Seq ID	Mögliche Deletionen (Δ) (AS-Position/AS-Anzahl)	Einfügestellen (Ω) von den Inserts (AS-Position/Seq ID)		
			Brückenbnd. 1,2,3 (Seq ID 1-3)	native Brückenbnd.1 (Seq ID 4)	Epitope (Seq ID 5-36)
gag (500 AS)	I.	Δ 1/131	Ω 132(1/3)	Ω 249(4)	
		Δ 159/150	Ω 249(2/3)	Ω 323(4)	
		Δ 363/14	Ω 323(1/2/3)	Ω 450(4)	
		Δ 450/50	Ω 450(1/2/3)		
pol 1 (561 AS)	II.	Δ 1/60	Ω 61(1/2/3)	Ω 61(4)	
		Δ 398/29	Ω 228(1/2/3)	Ω 284(4)	
		Δ 441/120	Ω 284(1/2/3)	Ω 436(4)	
			Ω 436(1/2/3)	Ω 535(4)	
			Ω 535(1/2/3)		
pol 2 (289 AS)	III.	Δ 100/40	Ω 31(1/2)	Ω 140(4)	
		Δ 163/14	Ω 100(1/2/3)	Ω 177(4)	
			Ω 140(2/3)		
			Ω 177(1/3)		
env 1 (491 AS)	IV.	Δ 1/4	Ω 44(1/2/3)	Ω 87(4)	Ω 3(14/17/29-36)
		Δ 54/18	Ω 87(1/2/3)	Ω 160(4)	Ω 75(13-20/24/27/31)
		Δ 136/1	Ω 160(1/2/3)	Ω 253(4)	Ω 136(13-36)
		Δ 230/20	Ω 253(1/2/3)		Ω 137(13-25/35)
		Δ 489/2	Ω 417(1/2/3)		Ω 213(13-18/23-36)
env 2 (392 AS)	V.	Δ 1/46			Ω 392(13-36)
		Δ 142/13	Ω 8(1/2)		Ω 452(19/21/34)
		Δ 210/5	Ω 112(1/2/3)		Ω 8(5-8/9/11/12)
		Δ 240/23	Ω 215(1/2/3)		Ω 45(9-11)
		Δ 344/48	Ω 344(1/3)		Ω 161(5/7/8)
env 3 (360 AS)	VI.	Δ 2/38	Ω 69(1/2/3)		Ω 202(6/7)
		Δ 257/103	Ω 176(1/2/3)		Ω 214(6-8)
			Ω 253(1/2/3)		Ω 215(9-12)
					Ω 286(10/11)
					Ω 344(9-12)

2. Aminosäuresequenzen (Single Letter Aminosäurecode) der Insertionen

Seq ID	Aminosäuresequenz	Seq ID	Aminosäuresequenz
1	GKR--K-RK-KR--RRG	20	IRQGIHIGPGRAFFAAW
2	G-KK-RR-KGK-RR-KK-G	21	DVQEMRIGPMAWYSMG
3	G-C-K-R-KRRRRK-K--C-G	22	ICTRRGIRMGPGQVVYATCT
4	GVA--K-KRR---REKRAVG	23	TIVQIKIIGPLAVYSMYG
5	WIQLQRLNLWGCRGKLCYTN	24	TRKSVRIGPGQAFYAT
6	WIQNQQLNLWGCKGRLVICYTN	25	GHTRKSIRIGPGQTFYAT
7	WLQNQQIILNLWGCKGRLCYTN	26	NTRQSTHIGPGALYTTKIE
8	WLQSQQLLSNWGCRGKLVICYTN	27	TRKSIHLGPGQAFYATGD
9	AIERYLQDQARLNSWGCFTFRQVCH	28	YQTRKSIRIGPGQAFYATGD
10	AMEKYLRDQAIVNSWGCAFRQVCY	29	TVQEIRIGPMAWYSMGNV
11	AMEKYLKDQARLNSWGCAFRQVCH	30	TRISHTIGPGRVFYRT
12	AI EKYLKHQAQLNAWGCAFRQVCH	31	TRKGIHMGPGQVLYATKP
13	TRKSIHIGPGQAFYATGD	32	HTRKSIHIGPGRAFYATS
14	TRRSISFGIGPGQALYTT	33	TRKSIHIGPGRAFYTTSMQ
15	TRQRTPIGLGQALYTTGQF	34	QTRTSITIGPGQVFYRTE
16	RTVQEIRIGPMAWYSMGA	35	GTRKSVRIGPGQTFYATG
17	TMKRTSIHIGPGQTFYAT	36	TRKGIHIGPGRAFYATG
18	TRRGIPLGPGRAWYATL	37	AVGIGINCTRPNNN
19	DSTRESMRIGPGQAFYATG	38	GDIIGDIRQAHCNIGTPTT

Legende: X ≡ D oder E
 "- " ≡ beliebige Aminosäure

Patentanhang

Fig. 1

1. Aminosäuresequenzen (Single Letter Aminosäurecode)

Seq ID I.: gag (500 AS)

M¹GARASVLSGGELDRWEKIRLRPGGKKKYK¹LKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEIKDTK
EALDKIEEEQNKKKKAQAAADTGHSNQVSQNY¹PIVQNIQGMVHQAI¹SPRTLNAWVKV¹EEKAFSPEV¹IPMSALSEGATPQDLN¹TML
NTVGGHQAAMQMLKETINEEAAEWDVRVHPVHAGPIAPGOMREPRGSDIAGTSTLQEQIGW¹MTNNPP¹IPVGEIYKRWIILGLNKIVRMYSPTSI
LDIRQGPKEPFRDYDRFYKTLRAEQ¹AEVKNWMTETLLV¹QANANPDCKTILKALGAATLEEMMTACQGVGGPGHKARVL¹AEAMSQV
TNSATIM¹MQRGNFRNQKIVKFCNCGKEGHTARNCRAPRKKGCKGKEGHOMKDC¹TERQANFLGKIWPSYKGRPGNFLO¹SRPEPTAP
PEESFRSGVETTPPQKEPIDKELYPLTSLRSLFGNDPSSQ¹

Seq ID II.: pol 1 (561 AS)

M¹PISPIETVPVKLPGMGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPV¹FAIKKKDSTKWRKLVDFRELNKR¹TQDEFW
EVQLGIPHPAGLKKKKS¹VTLDVGDAYFSVPLDEDFERKYTAFTIP¹SINNETPGIRYQYNVL¹PQGWKGS¹PAIFQSSMTKILEPFRKQNP¹NIVYQYMD¹DL
YVGS¹DL¹EIGQHR¹TKIEELRQHL¹LRWGLTTPDKKHQKEPPF¹LMWGYELHPDKWTVQPIVL¹PEKDSWTVNDIQKLVGKLNWASQI¹YPGIKVRQL
CKLL¹PRG¹TKALTEV¹IPLT¹EEAELELAENREILKEPVHGVY¹YDPSKDLIAEIQKQCGQW¹TYQIYQEPFKNLKTGKYARMGAHTNDVKQLTE
AVQKITTESIV¹WGT¹PKFKLPIQKET¹WETWWT¹EYWQATWIP¹EWEFVNT¹PPLVKLW¹YOLEKEPIV¹GAET¹FYVDGAANRET¹KLKGAGYVT
NRGRQKV¹TLTDT¹TNQKTELQAIYLAIQDSGLEVNI¹VTDSQYALGIIQAQPDQSESELVNI¹IEQLIKKEKVYLA¹WVPAHKGIGGNEQVDKL
VSAGIRKVL¹

Seq ID III.: pol 2 (289 AS)

MFLDGIDKAQDEHEKYHSNW¹RAMASDFNLPP¹VVAKEIVASCDK¹QKLG¹EAHMGQVDCSPGIWQLDCTHLEGVILVAVHVASGYIEAEVIPA
ETGQETAY¹FLLKLAGRWPVKT¹IHTDNGSNFTSATVKAACWAGIKQEF¹GI¹PNPQSQGVV¹ESMNKELK¹IGQVRDQAEH
LKTAV¹QMAVFIH¹NFKRKGIGGYSAGERIVDI¹IATDIQTKELQKQITKIQNFRVY¹YRDSRNP¹LWKGPAKLLWKGEGAV¹IQD¹NSDIKVVPR
RKAKIIRDYGKQAGDDCVASRQDE¹

Seq ID IV.: env 1 (491 AS)

M¹DC¹⁴14/17/29-36+SH¹G¹TEKLWTVVYGVVWKEATTLFCASDAKAY¹DTEVHNV¹1/2/3+WATHACVPTD¹PNPQEVVLNVVTENFNMW¹
¹KND¹13-20/24/27/31+MVEQMHE¹II¹SL¹1/2/3+WDQSLKPCVKLTPLCVSLKE¹CTDLKNDTNTNSSGRMIMEKEIKNC¹1/2/3+P¹
¹13-25/35+NIST¹SIRGKVQKEYAFFYKLDI¹1/2/3+PIDNDTTSYKLTSCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNKTFNGT¹13-18
¹1/23-36+GPC¹TNVSTVQCTHGIR¹PPVSTQLLLNGSLAEEVVI¹RSV¹1/2/3+NFTDNAKTIIVQLNTSVEINCTRPNNNTRKRIRIQRGPGRAFT¹
¹IGKIGNMRQAH¹CNISRAKNNTLKQIASKLREQFGNKTII¹FKQSSGGDPEIVTHSFNCGGEFFYCNS¹TQLENSTWFNSTWSTEGSNNT¹EGSD¹1/2
¹3-36+TITLPCRIKQIINMWQVKGKAMYAP¹1/2/3+PISQIRCSSNITGLLLTRDGGNSNNESEIFRPGG¹19/21/34+GDMRDNRSELYKYKV¹
¹KIEPLGVAPTAKRRVVQRE¹KK¹

Seq ID V.: env 2 (392 AS)

M¹GSDMRDN¹1/2/5-8/9/11/12+WRSELYKYKVVKIEPLGVAPTAKRRVVQREKRAVGIGS¹19-11+ALFLGLGAAGSTMGAASMTLLTVQA¹
¹ROLLSGIVQQONLLRAIEAQHLLQLTVGIKQLQARIL¹1/2/3+FAVERYLKDQQLGIWGC¹SGKLICTTAVPWN¹ASWSNKSLEQIWN¹NMTWME¹
¹1/5/7/8+WDREINNYTSLIHS¹LEESQ¹QKE¹NEQELLELDK¹WASLWN¹6/7+WFNITNWLP¹EFNN¹1/2/3/9-12+FYIKLFIMIVGG¹
¹LVGLRIVFAVLSI¹1/VNRVRQGYSPLSFQTHLP¹IPRGP¹DRPEGIEEGGERDRSIRLVN¹10/11+GSLALIWD¹DLRSCLCFSYHRLRDL¹LLIVT¹
¹RIVELLGRRGWEALKYWNLLQYWSQELK¹1/3/9-12+NSAVSLLNATAIAVAEGTDRVIEVVQACRAIRHIPRIRQGLERILL¹

Seq ID VI.: env 3 (360 AS)

MM¹SSAHGRHTRGVFLGFLGFLATAGSAMGAASLT¹VSQA¹RTLLAGIVQQQQQLLDVVKRQQLRLTV¹1/2/3+WG¹TKNLQARVTAIEKYLQDQA¹
¹RLNSWGCAFRQVCHTTPVWVND¹SLAPDWDNMTQEW¹QVRYLEANI¹SKSLEQAQIQ¹QEK¹NMYELQK¹LN¹SWDIFGNWFDLT¹SWVK¹1/2/3+FYIQY¹
¹VLIIVAVIALRIVIVVQMLSR¹LKGYRPFSSPPGYIQ¹QI¹HKDRGQ¹SPANEE¹TEEDGGSNGGDRYWPWP¹1/2/3+IAYI¹HFLIRQLIRLLTRL¹
¹YSICRDLRSF¹TLQLIYQNL¹RDWLR¹LRTAFLQYGC¹EWIQEAFQAAARATRETLAGACRGLWRVLERIGRILAVPRRIRQGA¹EIAL¹

Legende: ¹ bzw. ¹ ≡ Anfang bzw. Ende einer möglichen Deletion

¹A/B¹ ≡ Mögliche Einfügestellen (Insertionsstellen) einer AS-Sequenz mit der Seq ID A und/oder B

4. Beispielproteine aus der Permutationstabelle (A, B und C) und andere (D und E)

A. pol 2 Δ 100/40, 140/23, 163/14 Ω 31/2, 100/3 (253 AS)

MFLDGIDKAQDEHEKYHSNWRAMASDFNLPPGPKARRIKGKMRRVKAGVVAKEIVASCDKQCKEAMHGQVDCSPGIWQLDCTHLEGGKVLVAVHV
ASGYIEAEVIPAETGQETAYGACIKHRYKRRDRRHKKVACIGQMAVFIHFKRKGIGGYSAGERIVDIIATDIQTKELQKITKIQNFVYVYRDSRNP
LWKGPAKLLWKGEAVVIQDNSDIKVVPRRKAKIIRDYKGQMGAGDDCVASRQDED

B. env 2 Δ 47/25, 210/5, 215/25, 240/23, 286/58, 344/48 Ω 215/11 (232 AS)

MGSDMRDNWRSELYKYKVVKIEPLGVAPTAKRRVVQREKRAVGIGSRQLLSGIVQQNNLLRAIEAQHLLQLTVWGIKQLQARILAVERYLKDQQLL
GIWCGSGKLICTTAVPWNASWSNKSLEQIWNMTWMEWDREINNYTSLIHSLEESQNEQELLEDKQWASLWNWFNITNWLAMEKYLKQDQARLN
SWGCAFRQVCHDRPEGIEEGGERDRDRSIRLVN

C. env 2 Δ 47/25, 210/5, 215/25, 240/23, 286/58, 344/48 Ω 8/6, 215/11 (254 AS)

MGSDMRDNWIONQQLNLWGCKGRVLCYTNWRSELYKYKVVKIEPLGVAPTAKRRVVQREKRAVGIGSRQLLSGIVQQNNLLRAIEAQHLLQLTVW
GIKQLQARILAVERYLKDQQLLGIWCGSGKLICTTAVPWNASWSNKSLEQIWNMTWMEWDREINNYTSLIHSLEESQNEQELLEDKQWASLW
NWFNITNWLAMEKYLKQDQARLNSWGCAFRQVCHDRPEGIEEGGERDRDRSIRLVN

D. AS(M) + Seq ID (1+37+24+38+2+37+32+38+3+37+27+38+2+37+25+38+1) (297 AS)

MKRAHKSRIKRVTRRGAVGIGINCTRPNNNTRKSVRIGPGQAFYATGDIIGDIRQAHNCNIGPTPTGWKKNNRRLKGKYRRMKKWGAVGIGINCTRPNN
NHTRKSIHIGPGRAFATSGDIIIGDIRQAHNCNIGPTPTGACVKKRQKRKEKRYKTACVGAAGVIGINCTRPNNNTRKSIHLGPGQAFYATGDDIIGDI
RQAHNCNIGPTPTGSKKARRIKGMMRRLKKGAVGIGINCTRPNNNGHTRKSIRIGPGQTFYATGDIIGDIRQAHNCNIGPTPTGKRAVKSRYKRHIRRG

E. env 4 (221 AS)

MGSDMRDNWRSELYKYKVVKIEPLGVAPTAKRRVVQREALETLQNQQILNLWGCKGRILCYWGIKQLQARILAVERYLKDQQLLGIWCGSGKLICTT
AVPWNASWSNKSLEQIWNMTWMEWDREINNYTSLIHSLEESQNEQELLEDKQWASLWNWFNITNWLAIKYLKQDQARLNSWGCAFRQVCHDR
PEGIEEGGERDRDRSIRLVNGS

5

5

R Q V
 F A H HD R P
 WG NS
 OARL
 YLKD
 AMEK
 TNWL
 WFNI
 LNNW
 ASWS
 WASN
 ELDK
 EQELL
 E
 SONOCEKN
 RDRDRSIRLVINGS

NI TROZELLULOSEMBRAN

→ 4. D.: AS(M) + Seq ID (1+37+24+38+2+37+32+38+3+37+27+38+2+37+25+38+1)

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<- Epitop ->
GPGOA
RI FYA TGD
KSV TR IIG DI
NN PN RQ
TR AH
E--E
AVGIGIN NIGPTPT
GKRAHK:SRKIKRVTRG
<- pos. Brücke ->

<- Epitop ->
PGRAFY
HIG ATS
KSI GD
TR IIG DI
NNH DI
PN RQ
TR AH
E--E
AVGIGIN NIGPTPT
GACVKHROKKEKRYKTACVG
<--- pos. Brücke --->

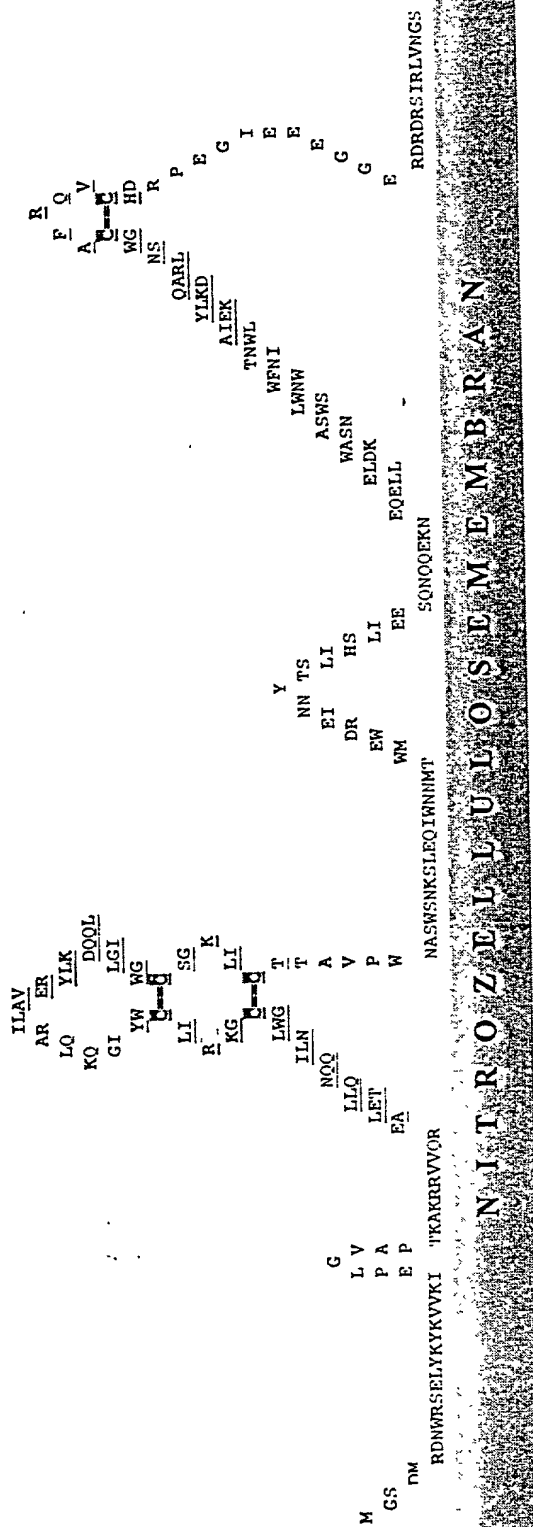
<- Epitop ->
GPGQAFYA
IHL TGD
KS GD
TR IIG DI
NN DI
PN RQ
TR AH
E--E
AVGIGIN NIGPTPT
GSKARRIKGMRLKVG
<-- pos. Brücke -->

<- Epitop ->
GPGQTFY
IRI AT
RKS GD
GHT IIG
NN DI
PN RQ
TR AH
E--E
AVGIGIN NIGPTPT
GKRAVK:SKYKRHRIRG
<- pos. Brücke ->

```

NITROZEN LULLOSETMEMBRAN

B. Negatives Beispiel (4.E.): env 4



- Legende:
- Aminosäure in rot ≡ positiv geladene Aminosäure
 - Aminosäure in blau ≡ negativ geladene Aminosäure
 - Aminosäure in grün ≡ polare Aminosäure
 - Brückenbindung von zwei Cysteinen ≡